

Research fronts of agriculture in 2023

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At the end of 2023, Chinese Academy of Sciences (CAS) and Chinese Academy of Engineering (CAE) successively announced “2023 Research Fronts”^[1] and “2023 Engineering Fronts”^[2,3], respectively. Among them, agricultural sciences occupy a pivotal position on both fronts.

1 “2023 Research Fronts” in agriculture of CAS

The “Research Fronts” of CAS can be traced back to 2013. In 2013, Clarivate published an inaugural report in which 100 hot research fronts were identified. Since then, CAS and Clarivate jointly released a succession of annually updated “Research Fronts” reports. These reports have gained widespread attention from around the world.

The research fronts of CAS were selected from two aspects, namely “hot research fronts” and “emerging research fronts”. The specific methodology used for identifying the research fronts is described in the report “2023 Research Fronts”^[1]. According to the Research Leadership Index (RLI_{Ci}) reported in “Research Fronts 2023: Active Fields, Leading Countries/Regions”, it is noteworthy that the Chinese mainland has outstanding performance and ranks first in agriculture^[4].

1.1 Hot research fronts

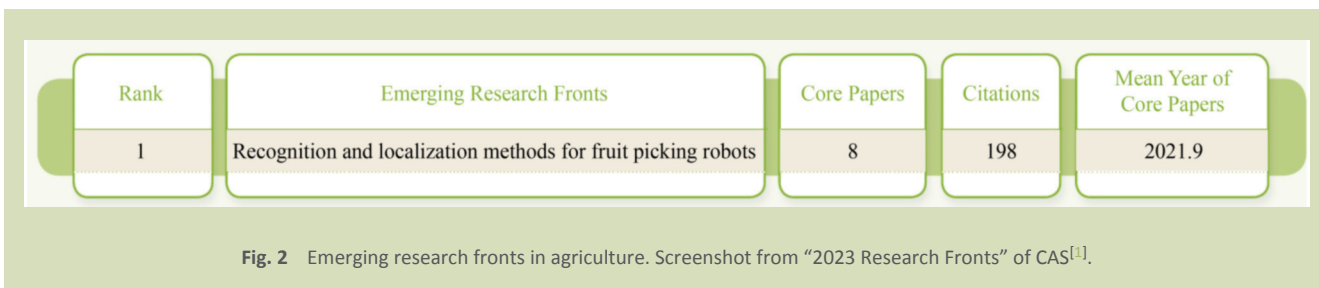
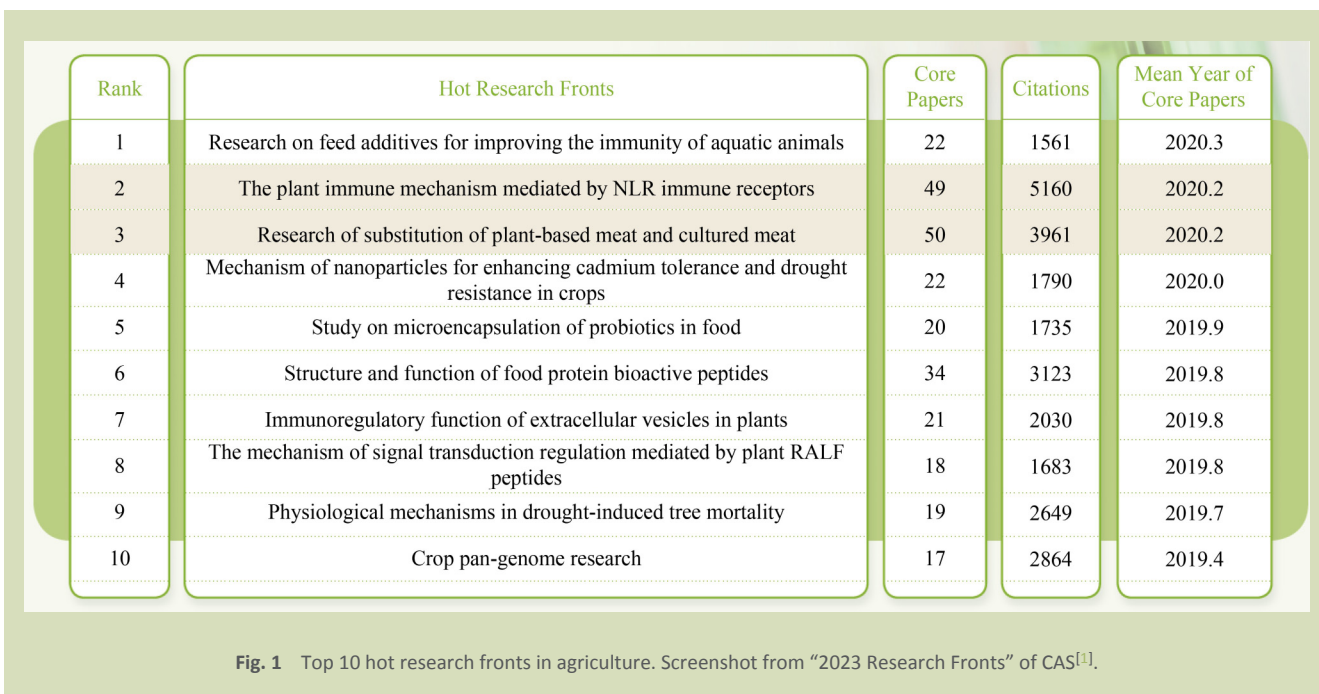
In 2023, the Top 10 hot research fronts in agriculture were reported (Fig. 1). Compared with previous “Research Front”

surveys, some research has been ongoing for a decade and has registered frequently in previous Top 10 lists for many years. Notably, both crop pan-genome research in the subfield of plant genome, and the plant immune mechanism mediated by NOD-like receptor (NLR) immune receptors in the subfield of plant immune regulation, have continuously appeared in the “Research Front” roundup for three years since 2021. Meanwhile, the current high research interest in the substitution of plant-based meat and cultured meat has made it into the Top 10 lists for the first time^[1].

1.2 Emerging research fronts

A “Research Front” with core papers of recent vintage indicates a specialty with a young foundation that is rapidly growing. To identify emerging specialties, the immediacy of the core papers is a priority, and that is why it is characterized as “emerging”. In 2023, one emerging research front has been identified in agriculture, which is “recognition and localization methods for fruit picking robots” (Fig. 2).

The report provides a brief and clear interpretation of this emerging research front, excerpted as follows. A picking robot is a flexible automated or semi-automatic device that operates on fruits or vegetables. It combines partial human information perception and limb movement functions and can be repeatedly programmed. It is an intelligent machine that integrates various disciplines such as electronics, machinery, computers, sensing technology, control technology, artificial intelligence, bionics, and agriculture. Using picking robots instead of human labor can not only reduce labor intensity but



also improve labor efficiency and help solve the problem of labor scarcity. Therefore, the picking robot has garnered attention from developed countries with relatively small agricultural workforces and has become one of the competitive focuses of international agricultural machinery technology. For picking robots, especially fruit-picking robots, the complex natural conditions in which the fruits are located often lead to the situation that the fruit is obstructed by branches and leaves or overlapped with other fruits. This significantly hinders the recognition of machine vision systems. Therefore, the methods for fruit recognition and positioning in fruit-picking robots have become a hot research topic^[1].

Compared with the hot research fronts in the past five years, the research on the plant immune mechanism mediated by NLR immune receptors has been included in the Top 10 lists for three consecutive years, ranking gradually higher, and has been elaborated as a key hot research front content in 2023. Close to half of the core papers on this hot frontier topic have

been published in *Cell*, *Science*, or *Nature* and their sub-journals. The top producer of core papers is China, followed by Germany and USA in second and third place, respectively. It shows that Chinese scientists have made outstanding achievements in this field^[1,5–8].

The crop pan-genome research has been selected as the hot research front in 2021 and 2023, and has been interpreted in detail as the key hot research front in 2021^[1,6]. The concept of pan-genome was first proposed in the field of microbiomics in 2005, mainly by Herve Tettelin of University of Maryland^[9]. This concept was then quickly applied to the field of animal, and was soon expanded and applied to the field of animal and plant genomics, leading genome research into the era of pan-genomics^[6]. Among the Top 10 countries and institutions producing this front’s core papers, Australia can boast the highest contribution, China ranks second, and USA ranks third. Among the prolific contributing institutions, Chinese Academy of Agricultural Sciences (CAAS) in China ranks

second with a contribution rate of 31.3%. In terms of countries that cite the core papers in this hot front, China, which ranks second in the output of core papers, makes the largest contribution, accounting for nearly 44%. In terms of awarding institutions, CAAS, CAS, and Huazhong Agricultural University (HZAU) ranked the Top three in order.

In terms of RLI_{Ci} in the area of “Agricultural, Plant and Animal Sciences”, China ranked second in 2019 and first in 2020–2023. The two powerful nations of China and USA have solid positions. China has significant advantages and the most active performance, ranking at the forefront for the past five years^[1,5–8].

2 “2023 Engineering Fronts” in agriculture of CAE

Since 2017, CAE has been organizing a project known as “Global Engineering Fronts” every year, which aims to assemble talents in the field of engineering science and technology to resent the global engineering research and development fronts by reviewing global papers, patents, and other data. The results are also expected to provide a reference for people to respond to global challenges and achieve sustainable development^[2,3].

CAE “Global Engineering Fronts” identifies and releases nearly two hundred of “engineering research fronts” and “engineering development fronts” every year to guide academic development and promote the innovation of engineering science and technology. On agriculture fronts, CAE has set up a team composed of 11 disciplines which are crop breeding, crop cultivation, horticultural crops, plant protection, resource ecology, animal breeding, animal nutrition, animal medicine, agricultural engineering, forestry science, and aquatic science. CAE invites international and domestic academicians and experts from different disciplines to actively give advice and suggestions both online and offline participation. Online participation for agriculture fronts was achieved through the website of *Frontiers of Agricultural Science and Engineering* (FASE) and emails.

2.1 Engineering research fronts

In 2023, the Top 10 engineering research frontiers in the field of agriculture released by CAE are shown in Fig. 3. It is noteworthy that crop pan-genome ranks first in 2023, it is expected to serve as a uniform and comprehensive coordinate system for facilitating gene mining and molecular design breeding, ultimately accelerate the crop basic research and development of improved varieties for ensuring national food security and sustainable agricultural development.

No.	Engineering research front	Core papers	Citations	Citations per paper	Mean year
1	Crop pan-genome	50	11270	225.40	2017.7
2	Mechanisms and methods for synergistic improvement of crop yield, quality, and efficiency	43	3684	85.67	2018.5
3	Genetic basis and regulatory network for the quality formation of horticultural crops	58	3321	57.26	2018.6
4	Intelligent identification mechanism and real-time monitoring technology for crop diseases and pests	42	4876	116.10	2019.2
5	Straw modification and rapid decomposition technology	67	1939	28.94	2019.8
6	Mechanisms of host inflammatory response regulation mediated by significant animal pathogens	54	2603	48.20	2018.3
7	Antibiotic-free nutritional regulation techniques for the intestinal health and growth of livestock and poultry	35	2313	66.09	2019.1
8	Functional gene identification by multi-omics in animals	50	2645	52.90	2018.2
9	Intelligent collaborative operation technology for multiple agricultural machinery	40	3615	90.38	2019.2
10	Diagnosis of forest diseases and pests based on deep learning	18	1340	74.44	2019.3

Fig. 3 Top 10 engineering research fronts in agriculture. Screenshot from “2023 Engineering Fronts” of CAE^[2,3].

2.2 Engineering development fronts

In agriculture, there are Top 11 engineering development fronts published in 2023, mainly involves directions such as agricultural green development, smart agriculture and agricultural engineering, and reflect interdisciplinary applications (Fig. 4). It can be known from these fronts that gene editing technology is a hot research topic for researchers, such as “key technologies for unmanned farms” and “ecological breeding technology of aquatic animals”. Genome editing has been a hot research topic for many years^[9]. Furthermore, agricultural green development has received widespread attention from researchers in recent years.

3 Crop pan-genome

The concept of pan-genomes was first developed in bacteria and proposed by Tettelin et al.^[9] in 2005, it means a collection of all DNA sequences of a species. Pan-genomes represent the genomic diversity of a species and includes core genes, found in all individuals, as well as variable genes, which are absent in some individuals^[10].

In recent years, crop pan-genomics has emerged as a crucial area of research within the field of crop genomics. It offers valuable insights into the genetic variations, evolutionary origins, and functional genes of crops. In terms of staple crops like maize, rice, and wheat, the utilization of multiple high-quality reference genomes has gained momentum. This

approach has proven more effective in capturing the genetic diversity of the species compared to relying on a single reference genome. Specifically, the utilization of multiple genome assemblies from different individuals or varieties has revealed a wealth of structural variations, including tandem repeats, presence/absence variations, and chromosome translocations. This approach ensures a more comprehensive and accurate understanding of the genetic makeup of these staple crops. Constructing a pan-genome at the genus level will provide valuable evidence for understanding crop origin and evolution, decoding the domestication and de-domestication process, and revealing the evolution process of functional genes. Moreover, integrating the resourceful sequence information provides the opportunity for resolving the core genes and dispensable genes at the pan-genome level, promoting the mining and exploiting of beneficial gene recourses.

Recent pan-genome studies in human and plant species have uncovered species-wide biodiversity with an emphasis on the characterization of structural variants (SVs)^[10–14]. Additionally, increasing studies have focused on the construction of graph-based genomes in which loci with common variants are represented by alternative sequences. Therefore, graph-based genomes contain not only reference sequences but also variants in a population, providing a promising approach for pan-genome representation^[15–18]. Based on this, Li et al.^[19] reported a graph-based cucumber pan-genome by analyzing 12 chromosome-scale genome

No.	Engineering development front	Published patents	Citations	Citations per patent	Mean year
1	Development and application of genome editors in crops	4658	63027	13.53	2020.3
2	Crop green super-high-yield cultivation technology	181	437	2.41	2019.7
3	Development and utilization of high-quality germplasm resources for horticultural crops	88	137	1.56	2020.3
4	Molecular design of green pesticides based on structural biology	111	2177	19.61	2018.8
5	Synergistic technology for efficient conversion of organic matter and reduction of pollutants during composting	797	6983	8.76	2018.9
6	Creation of novel and efficient animal vaccines	52	119	2.29	2019.0
7	Preparation of feed by pre-digestion fermentation bioprocessing	73	76	1.04	2019.3
8	Genomic mating breeding technology for livestock and poultry	856	1587	1.85	2020.0
9	Key technologies for unmanned farms	1000	3541	3.54	2019.7
10	Bio-refinery of wood waste	46	71	1.54	2019.5
11	Ecological breeding technology of aquatic animals	52	25	0.48	2020.6

Fig. 4 Top 11 engineering development fronts in agriculture. Screenshot from “2023 Engineering Fronts” of CAE^[2,3].

assemblies, the results showed that genotyping of seven large chromosomal rearrangements based on the pan-genome provided useful information for use of wild accessions in breeding and genetic studies. The graph-based cucumber pan-genome and the identified genetic variants provide rich resources for future biological research and genomics-assisted breeding.

The achievement of super-high-quality genome assemblies, such as gap-less genome and telomere-to-telomere complete genome assemblies provide strong guidance in constructing crop pan-genomes in recent years. The methodological method and analysis approaches based on pan-genomes are unceasingly improving, and tasks such as the sequence mapping on pan-genome, functional annotation of gene family, and constructing graph-based pan-genomes are calling for technical innovations. In the future, incorporating advanced technologies, such as artificial intelligence and machine learning, and abundant phenotype data, the crop pan-genomics is expected to serve as a uniform and comprehensive coordinate system for facilitating gene mining and molecular design breeding, ultimately accelerating the crop basic research and development of improved varieties for ensuring national food security and sustainable agricultural development^[2].

As journal editors, we are concerned about the publication and citations of articles on relevant topics as well. We searched the Web of Science Core Collection for articles on the topics of “pan-genome” and “soybean or maize or cotton or rice or potato or oilseed rape or wheat or Chinese cabbage or crop” from 2019 to now (April 8, 2024) and found 317 results. The number of articles published on the topic of crop pan-genome

has increased year by year from 2019 to 2022, same as the citation number. The number of published crop pan-genome topic articles was 17 in 2019, increased by 76% to 30 in 2020, 107% to 62 in 2021, and 6% to 66 in 2022, respectively (Fig. 5). The number of crop pan-genome articles published in 2023 was 56, this is likely due to a delay in Web of Science inclusion, with many articles published in the fourth quarter of 2023 not yet included in the database. The citations in 2023 were 2124, an increase of 20% than in 2022. The data for 2024 appears to be low as the year has just commenced and comprehensive data statistics are not yet available.

Considering the distribution of articles by country, it can be seen that the main contributors of core papers on the “crop pan-genome” were China (48.16%), USA (31.43%), and Australia (18.37%) (Table 1).

The distribution of articles by research institution shows that the highest is CAAS (14.67%), the percentage of core papers is same (8.98%) for United States Department of Agriculture (USDA) and University of Western Australia (UWA), ranked in second and third, respectively (Table 2).

As for the contribution of citing articles by country, it can be seen that the main country with the greatest output of citing papers on “crop pan-genome” is China (46.34%), followed by USA (22.80%) and Australia (11.41%) (Table 3).

The distribution of citing articles by research institution shows that the first three institutions are CAAS (11.33%), CAS (6.94%), and Ministry of Agriculture Rural Affairs (MARA) of the People’s Republic of China (6.29%) (Table 4).

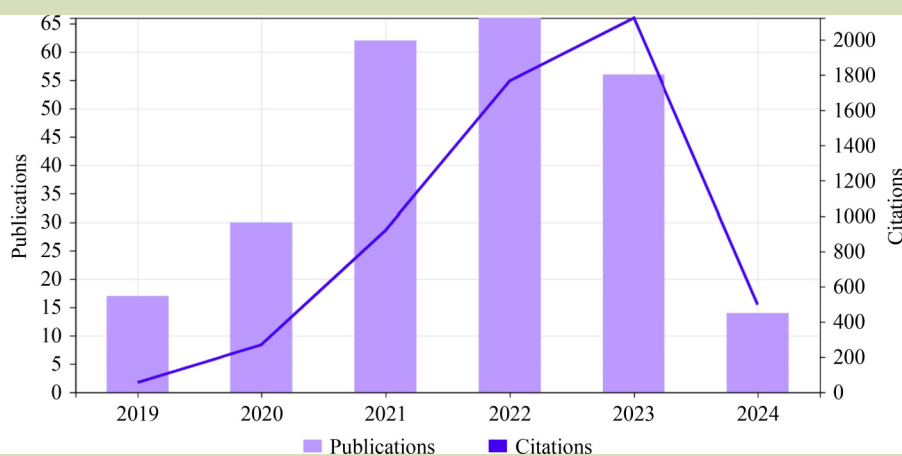


Fig. 5 Number of published articles and citations on “crop pan-genome”. Data sourced from Web of Science and collected on April 8, 2024.

Table 1 Countries with the greatest output of core papers on “crop pan-genome”

No.	Country	Core papers	Percentage of core papers
1	China	118	48.16%
2	USA	77	31.43%
3	Australia	45	18.37%
4	India	37	15.10%
5	Germany	28	11.43%
6	UK	16	6.53%
7	Canada	15	6.12%
8	Pakistan	11	4.49%
9	Italy	9	3.67%
10	Saudi Arabia	9	3.67%

Note: Data sourced from Web of Science and collected on April 8, 2024.

Table 2 Institutions with the greatest output of core papers on “crop pan-genome”

No.	Institution	Core papers	Percentage of core papers
1	Chinese Academy of Agricultural Sciences (CAAS)	36	14.67%
2	United States Department of Agriculture (USDA)	22	8.98%
3	University of Western Australia (UWA)	22	8.98%
4	Chinese Academy of Sciences (CAS)	21	8.57%
5	CGIAR	20	8.16%
6	Indian Council of Agricultural Research (ICAR)	18	7.35%
7	University of California System (UCS)	17	6.94%
8	Huazhong Agricultural University (HZAU)	16	6.53%
9	Institute of Crop Sciences, CAAS	15	6.12%
10	Ministry of Agriculture Rural Affairs (MARA) of the People’s Republic of China	15	6.12%

Note: Data sourced from Web of Science collected on April 8, 2024.

Table 3 Countries with the greatest output of citing papers on “crop pan-genome”

No.	Country	Citing papers	Percentage of citing papers
1	China	1657	46.34%
2	USA	815	22.80%
3	Australia	408	11.41%
4	India	323	9.03%
5	Germany	313	8.75%
6	UK	187	5.23%
7	France	138	3.86%
8	Canada	135	3.78%
9	Italy	127	3.55%
10	Spain	111	3.10%

Note: Data sourced from Web of Science collected on April 8, 2024.

Table 4 Institutions with the greatest output of citing papers on “crop pan-genome”

No.	Institution	Core papers	Percentage of core papers
1	Chinese Academy of Agricultural Sciences (CAAS)	405	11.33%
2	Chinese Academy of Sciences (CAS)	248	6.94%
3	Ministry of Agriculture Rural Affairs (MARA) of the People’s Republic of China	225	6.29%
4	United States Department of Agriculture (USDA)	219	6.12%
5	Huazhong Agricultural University (HZAU)	211	5.90%
6	Institute of Crop Sciences, CAAS	148	4.14%
7	CGIAR	145	4.06%
8	University of Western Australia (UWA)	140	3.92%
9	Indian Council of Agricultural Research (ICAR)	125	3.50%
10	University of Chinese Academy of Sciences (UCAS)	121	3.38%

Note: Data sourced from Web of Science collected on April 8, 2024.

4 Conclusions

The results of CAS and CAE reports and the Web of Science data show that crop pan-genomic is indeed a cutting-edge and hot topic of scientific research. The development of journals needs the support of high-quality and frontier scientific research articles, and the topic of crop pan-genome is worthy of reference and consideration by FASE journal.

We warmly invite researchers in the field of pan-genomics to

submit their papers or contribute review articles to FASE journal. In the future, all relevant articles in this field will be curated and assembled into a dedicated online special issue, providing a platform for scholars to exchange knowledge and insights. Moreover, we encourage experts and scholars who are interested in organizing special issues for FASE journal to actively sign up as guest editors for a specialized pan-genomics research issue, aiming to foster the sharing and dissemination of cutting-edge research in the field of pan-genomics.

Compliance with ethics guidelines

Jianxiang Xu, Yunzhou Li, Jie Zhao, Liang Shi, Yinkun Yao, and Jingyue Tang declare that they have no conflicts of interest or financial conflicts to disclose. This article does not contain any studies with human or animal subjects performed by any of the authors.

REFERENCES

- Institute of Science and Development, Chinese Academy of Sciences (CASISD). 2023 Research Fronts. Available at CASISD website on February 2, 2024
- Engineering. 2023 Engineering Fronts. Available at Engineering Website on February 2, 2024
- Frontiers of Agricultural Science and Engineering (FASE). 2023 Engineering Fronts. *FASE website*, 2023. <https://journal.hep.com.cn/fase/EN/column/item962.shtml>
- “Research Fronts 2023: Active Fields, Leading Countries/Regions”. Available at CASISD website on February 2, 2024
- 2022 Research Fronts. Available at Jinling Institute of Technology (JIT) Library website on April 1, 2024
- 2021 Research Fronts. Available at JIT Library website on April 1, 2024
- 2020 Research Fronts. Available at JIT Library website on April 1, 2024
- 2019 Research Fronts. Available at JIT Library website on April 1, 2024
- Tettelin H, Masignani V, Cieslewicz M J, Donati C, Medini D, Ward N L, Angiuoli S V, Crabtree J, Jones A L, Durkin A S, Deboy R T, Davidsen T M, Mora M, Scarselli M, Margarit y Ros I, Peterson J D, Hauser C R, Sundaram J P, Nelson W C, Madupu R, Brinkac L M, Dodson R J, Rosovitz M J, Sullivan S A, Daugherty S C, Haft D H, Selengut J, Gwinn M L, Zhou L, Zafar N, Khouri H, Radune D, Dimitrov G, Watkins K, O’Connor K J B, Smith S, Utterback T R, White O, Rubens C E, Grandi G, Madoff L C, Kasper D L, Telford J L, Wessels M R,

- Rappuoli R, Fraser C M. Genome analysis of multiple pathogenic isolates of *Streptococcus agalactiae*: implications for the microbial “pan-genome”. *Proceedings of the National Academy of Sciences of the United States of America*, 2005, **102**(39): 13950–13955
10. Xu J X, Li Y Z, Yao Y K, Zhao J, Tang J Y, Feng Z X. Genome editing: a ground breaking research has been ranked top 10 engineering fronts from 2017 to 2021. *Frontiers of Agricultural Science and Engineering*, 2022, **9**(2): 309–311
11. Bayer P E, Golicz A A, Scheben A, Batley J, Edwards D. Plant pan-genomes are the new reference. *Nature Plants*, 2020, **6**(8): 914–920
12. Li R, Li Y, Zheng H, Luo R, Zhu H, Li Q, Qian W, Ren Y, Tian G, Li J, Zhou G, Zhu X, Wu H, Qin J, Jin X, Li D, Cao H, Hu X, Blanche H, Cann H, Zhang X, Li S, Bolund L, Kristiansen K, Yang H, Wang J, Wang J. Building the sequence map of the human pan-genome. *Nature Biotechnology*, 2010, **28**(1): 57–63
13. Gao L, Gonda I, Sun H, Ma Q, Bao K, Tieman D M, Burzynski-Chang E A, Fish T L, Stromberg K A, Sacks G L, Thannhauser T W, Foolad M R, Diez M J, Blanca J, Canizares J, Xu Y, van der Knaap E, Huang S, Klee H J, Giovannoni J J, Fei Z. The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor. *Nature Genetics*, 2019, **51**(6): 1044–1051
14. Alonge M, Wang X, Benoit M, Soyk S, Pereira L, Zhang L, Suresh H, Ramakrishnan S, Maumus F, Ciren D, Levy Y, Harel T H, Shalev-Schlosser G, Amsellem Z, Razifard H, Caicedo A L, Tieman D M, Klee H, Kirsche M, Aganezov S, Ranallo-Benavidez T R, Lemmon Z H, Kim J, Robitaille G, Kramer M, Goodwin S, McCombie W R, Hutton S, Van Eck J, Gillis J, Eshed Y, Sedlazeck F J, van der Knaap E, Schatz M C, Lippman Z B. Major impacts of widespread structural variation on gene expression and crop improvement in tomato. *Cell*, 2020, **182**(1): 145–161.e23
15. Tao Y, Luo H, Xu J, Cruickshank A, Zhao X, Teng F, Hathorn A, Wu X, Liu Y, Shatte T, Jordan D, Jing H, Mace E. Extensive variation within the pan-genome of cultivated and wild sorghum. *Nature Plants*, 2021, **7**(6): 766–773
16. Garrison E, Sirén J, Novak A M, Hickey G, Eizenga J M, Dawson E T, Jones W, Garg S, Markello C, Lin M F, Paten B, Durbin R. Variation graph toolkit improves read mapping by representing genetic variation in the reference. *Nature Biotechnology*, 2018, **36**(9): 875–879
17. Ameer A. Goodbye reference, hello genome graphs. *Nature Biotechnology*, 2019, **37**(8): 866–868
18. Liu Y, Du H, Li P, Shen Y, Peng H, Liu S, Zhou G A, Zhang H, Liu Z, Shi M, Huang X, Li Y, Zhang M, Wang Z, Zhu B, Han B, Liang C, Tian Z. Pan-genome of wild and cultivated soybeans. *Cell*, 2020, **182**(1): 162–176.e13
19. Li H, Wang S, Chai S, Yang Z, Zhang Q, Xin H, Xu Y, Lin S, Chen X, Yao Z, Yang Q, Fei Z, Huang S, Zhang Z. Graph-based pan-genome reveals structural and sequence variations related to agronomic traits and domestication in cucumber. *Nature Communications*, 2022, **13**(1): 682